SCORE Search Results Details for Application 10764201 and Search Result us-10-764-201-5.rge.

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This page gives you Search Results detail for the Application 10764201 and Search Result us-10-764-201-5.rge.

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                          GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:         August  3, 2006, 14:26:34 ; Search time 3380 Seconds
                                           (without alignments)
                                           8911.016 Million cell updates/sec

Title:          US-10-764-201-5
Perfect score:  471
Sequence:       1 atgcctaaaaaacgacggtc.....tcttccctggaacaacttag 471

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        GenEmbl:*
                 1:  gb_env:*
                 2:  gb_pat:*
                 3:  gb_ph:*
                 4:  gb_pl:*
                 5:  gb_pr:*
                 6:  gb_ro:*
                 7:  gb_sts:*
                 8:  gb_sy:*
                 9:  gb_un:*
                 10:  gb_vi:*
                 11:  gb_ov:*
                 12:  gb_htg:*
                 13:  gb_in:*
                 14:  gb_om:*
                 15:  gb_ba:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	463	98.3	1323	10	BLVTAP	M26772 Bovine leuk
2	414.6	88.0	927	10	AY700378	AY700378 Bovine le
3	414.6	88.0	8714	10	BLVCG	K02120 Bovine leuk
4	409.8	87.0	1474	10	BLV3TERM	M38278 Bovine leuk
5	403.4	85.6	3686	10	BLVENV	K02251 Bovine leuk
6	403.4	85.6	8419	10	AF033818	AF033818 Bovine le
7	401.8	85.3	927	10	AY700381	AY700381 Bovine le
8	400.2	85.0	1850	10	BLVORF	M26263 Bovine leuk
9	398.6	84.6	927	10	AY700380	AY700380 Bovine le
10	393.8	83.6	927	10	AY700382	AY700382 Bovine le
11	389.2	82.6	7933	10	BLVGPE	D00647 Bovine leuk
12	387.4	82.3	927	10	AY700379	AY700379 Bovine le
13	384.2	81.6	8588	10	AF257515	AF257515 Bovine le
14	112.4	23.9	180	10	BLVXREG2	M16018 Bovine leuk
15	70	14.9	70	2	AR070188	AR070188 Sequence
16	70	14.9	70	2	I21392	I21392 Sequence 20
17	68.4	14.5	70	2	AR070189	AR070189 Sequence
18	68.4	14.5	70	2	AR070190	AR070190 Sequence
19	68.4	14.5	70	2	AR070192	AR070192 Sequence
20	68.4	14.5	70	2	I21393	I21393 Sequence 21
21	68.4	14.5	70	2	I21394	I21394 Sequence 22
22	68.4	14.5	70	2	I21396	I21396 Sequence 24
23	66.8	14.2	70	2	AR070191	AR070191 Sequence
24	66.8	14.2	70	2	I21395	I21395 Sequence 23
25	58	12.3	805	10	AF399702	AF399702 Bovine le
26	56.4	12.0	1545	10	BLVENVE	M35242 Bovine leuk
27	54.8	11.6	960	10	AF111171	AF111171 Bovine le
28	54.8	11.6	1545	10	AF067081	AF067081 Bovine le
29	54.8	11.6	1545	10	BLVENVA	M35238 Bovine leuk
30	54.8	11.6	1545	10	BLVENVB	M35239 Bovine leuk
31	54.8	11.6	1545	10	BLVENVC	M35240 Bovine leuk
32	54.8	11.6	1548	10	AF399703	AF399703 Bovine le
33	54.8	11.6	1548	10	AF503581	AF503581 Bovine le
34	54.8	11.6	1548	10	AF547184	AF547184 Bovine le
35	54.8	11.6	1548	10	AY078387	AY078387 Bovine le
36	54.8	11.6	1548	10	AY151262	AY151262 Bovine le
37	53.6	11.4	7218	2	I66494	I66494 Sequence 14
38	51.6	11.0	1230	10	AY995174	AY995174 Bovine le
39	51.6	11.0	1548	10	AF399704	AF399704 Bovine le
40	51.6	11.0	1548	10	AY185360	AY185360 Bovine le
41	49.4	10.5	171	10	AY189711	AY189711 Bovine le
42	49.4	10.5	185	10	AY189714	AY189714 Bovine le
43	49.4	10.5	225	10	AY189710	AY189710 Bovine le
44	47.8	10.1	174	10	AY189715	AY189715 Bovine le
45	47.8	10.1	360	10	BLVXREG1	M16017 Bovine leuk

ALIGNMENTS

RESULT 1
BLVTAP

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LOCUS       BLVTAP                  1323 bp    mRNA    linear   VRL 28-APR-1993
DEFINITION  Bovine leukemia virus transactivator protein (XBL-1) mRNA, complete
            cds.
ACCESSION   M26772
VERSION     M26772.1  GI:210798
KEYWORDS    transactivator.
SOURCE      Bovine leukemia virus
  ORGANISM  Bovine leukemia virus
            Viruses; Retro-transcribing viruses; Retroviridae;
            Orthoretrovirinae; Deltaretrovirus.
REFERENCE   1  (bases 1 to 1323)
  AUTHORS   Rosen,C.A., Sodroski,J.G., Willems,L., Kettmann,R., Campbell,K.,
            Zaya,R., Burny,A. and Haseltine,W.A.
  TITLE     The 3' region of bovine leukemia virus genome encodes a
            trans-activator protein
  JOURNAL   EMBO J. 5 (10), 2585-2589 (1986)
   PUBMED   3023049
COMMENT     Original source text: Bovine leukemia virus, cDNA to viral RNA,
            clone pH3BLX.
FEATURES             Location/Qualifiers
     source          1. .1323
                     /organism="Bovine leukemia virus"
                     /mol_type="mRNA"
                     /db_xref="taxon:11901"
     CDS             316. .1245
                     /note="transactivator protein"
                     /codon_start=1
                     /protein_id="AAA42797.1"
                     /db_xref="GI:210799"
                     /translation="MASVVGWGPHSLHACPALVLSNDVTIDAWCPLCGPHERLQFERI
                     DTTLTCETHRINWTADGRPCGLNGTLFPRLHVSETRPQGPRRLWINCPLPAVRAQPGP
                     VSLSPFERSPFQPYQCQLPSASSDGCPIIGHGLLPWNNLVTHPVLGKVLILNQMANFS
                     LLPSFDTLLVDPLRLSVFAPDTRGAIRYLSTLLTLCPATCILPLGEPFSPNVPICRFP
                     RDSNEPPLSEFELPPIQTPGLSWSVPAIDLFLTGPPSPCDRLHVWSSPQALQRFLHDP
                     TLTWSELVASRKIRLDSPLKLQLLENEWLSRLF"
ORIGIN      3 bp upstream of XhoI site.

  Query Match             98.3%;  Score 463;  DB 10;  Length 1323;
  Best Local Similarity   98.9%;  Pred. No. 9.8e-123;
  Matches  466;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ATGCCTAAAAAACGACGGTCCCGAAGACGCCCACAACCGATCATCAGATGGCAAGTGTTG 60
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 ATGCCTAAAGAACGACGGTCCCGAAGACGCCCACAACCGATCATCAGATGGCAAGTGTTG 328

Qy         61 TTGGTTGGGGGCCCCACTCTCTACATGCCTGCCCGGCCCTGGTTTTGTCCAATGATGTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 TTGGTTGGGGGCCCCACTCTCTACATGCCTGCCCGGCCCTGGTTTTGTCCAATGATGTCA 388

Qy        121 CCATCGATGCCTGGTGCCCCCTCTGCGGGCCCCATGAGCGACTCCAATTCGAAAGGATCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 CCATCGATGCCTGGTGCCCCCTCTGCGGGCCCCATGAGCGACTCCAATTCGAAAGGATCG 448

Qy        181 ACACCACGCTCACCTGCGAGACCCACCGTATCAACTGGACCGCCGATGGACGACCTTGCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 ACACCACGCTCACCTGCGAGACCCACCGTATCAACTGGACCGCCGATGGACGACCTTGCG 508

Qy        241 GCCTCAATGGAACGTTGTTCCCTCGACTGCATGTCTCCGAGACCCGCCCCCAAGGGCCCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 GCCTCAATGGAACGTTGTTCCCTCGACTGCATGTCTCCGAGACCCGCCCCCAAGGGCCCC 568
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                                                                    119  120
Qy        301 GACGACTCTGGATCAACTGCCCCCTTCCGGCCGTTCGCGCTCAGCCCGGCCCGGTTAGAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db        569 GACGACTCTGGATCAACTGCCCCCTTCCGGCCGTTCGCGCTCAGCCCGGCCCGGTTTCAC 628
                                                                  Asp Phe His
Qy        361 CTTCCCCCTTCGAGCGGTCCCCCTTCCAGCCCTACCAATGCCAATTGCCCTCGGCCTCTA 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        629 TTTCCCCCTTCGAGCGGTCCCCCTTCCAGCCCTACCAATGCCAATTGCCCTCGGCCTCTA 688

Qy        421 GCGACGGTTGCCCCATTATCGGGCACGGCCTTCTTCCCTGGAACAACTTAG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        689 GCGACGGTTGCCCCATTATCGGGCACGGCCTTCTTCCCTGGAACAACTTAG 739
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